

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Jens Koßmann
- (B) STREET ADDRESS: Golmer Fichten 9
- (C) CITY: Golm
- (E) COUNTRY: DE
- (F) POSTAL CODE: 14476

(ii) TITLE OF INVENTION: Plants synthesizing a modified starch, methods for their production as well as modified starch

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER-READABLE VERSION:

- (A) DATA CARRIER: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4856 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Solanum tuberosum
- (B) STRAIN: C.V. Berolina

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 105..4497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CATCTTCATC GAATTTCTCG AAGCTTCTTC GCTAATTTC TGGTTTCTTC ACTCAAAATC	60
GACGTTTCTA GCTGAACTTG AGTGAATTAA GCCAGTGGGA GGAT ATG AGT AAT TCC	116
Met Ser Asn Ser	
1	
TTA GGG AAT AAC TTG CTG TAC CAG GGA TTC CTA ACC TCA ACA GTG TTG	164
Leu Gly Asn Asn Leu Leu Tyr Gln Gly Phe Leu Thr Ser Thr Val Leu	
5 10 15 20	
GAA CAT AAA AGT AGA ATC AGT CCT CCT TGT GTT GGA GGC AAT TCT TTG	212
Glu His Lys Ser Arg Ile Ser Pro Pro Cys Val Gly Gly Asn Ser Leu	
25 30 35	

TTT CAA CAA CAA GTG ATC TCG AAA TCA CCT TTA TCA ACT GAG TTT CGA Phe Gln Gln Gln Val Ile Ser Lys Ser Pro Leu Ser Thr Glu Phe Arg 40 45 50	260
GGT AAC AGG TTA AAG GTG CAG AAA AAG AAA ATA CCT ATG GAA AAG AAG Gly Asn Arg Leu Lys Val Gln Lys Lys Lys Ile Pro Met Glu Lys Lys 55 60 65	308
CGT GCT TTT TCT AGT TCT CCT CAT GCT GTA CTT ACC ACT GAT ACC TCT Arg Ala Phe Ser Ser Ser Pro His Ala Val Leu Thr Thr Asp Thr Ser 70 75 80	356
TCT GAG CTA GCA GAA AAG TTC AGT CTA GGG GGG AAT ATT GAG CTA CAG Ser Glu Leu Ala Glu Lys Phe Ser Leu Gly Gly Asn Ile Glu Leu Gln 85 90 95 100	404
GTT GAT GTT AGG CCT CCC ACT TCA GGT GAT GTG TCC TTT GTG GAT TTT Val Asp Val Arg Pro Pro Thr Ser Gly Asp Val Ser Phe Val Asp Phe 105 110 115	452
CAA GTA ACA AAT GGT AGT GAT AAA CTG TTT TTG CAC TGG GGG GCA GTA Gln Val Thr Asn Gly Ser Asp Lys Leu Phe Leu His Trp Gly Ala Val 120 125 130	500
AAA TTC GGG AAA GAA ACA TGG TCT CTT CCG AAT GAT CGT CCA GAT GGG Lys Phe Gly Lys Glu Thr Trp Ser Leu Pro Asn Asp Arg Pro Asp Gly 135 140 145	548
ACC AAA GTG TAC AAG AAC AAA GCA CTT AGA ACT CCA TTT GTT AAA TCT Thr Lys Val Tyr Lys Asn Lys Ala Leu Arg Thr Pro Phe Val Lys Ser 150 155 160	596
GGC TCT AAC TCC ATC CTG AGA CTG GAG ATA CGA GAC ACT GCT ATC GAA Gly Ser Asn Ser Ile Leu Arg Leu Glu Ile Arg Asp Thr Ala Ile Glu 165 170 175 180	644
GCT ATT GAG TTT CTC ATA TAC GAT GAA GCC CAC GAT AAA TGG ATA AAG Ala Ile Glu Phe Leu Ile Tyr Asp Glu Ala His Asp Lys Trp Ile Lys 185 190 195	692
AAT AAT GGT GGT AAT TTT CGT GTC AAA TTG TCA AGA AAA GAG ATA CGA Asn Asn Gly Gly Asn Phe Arg Val Lys Leu Ser Arg Lys Glu Ile Arg 200 205 210	740
GGC CCA GAT GTT TCT GTT CCT GAG GAG CTT GTA CAG ATC CAA TCA TAT Gly Pro Asp Val Ser Val Pro Glu Glu Leu Val Gln Ile Gln Ser Tyr 215 220 225	788
TTG AGG TGG GAG AGG AAG GGA AAA CAG AAT TAC CCC CCT GAG AAA GAG Leu Arg Trp Glu Arg Lys Gly Lys Gln Asn Tyr Pro Pro Glu Lys Glu 230 235 240	836
AAG GAG GAA TAT GAG GCT GCT CGA ACT GTG CTA CAG GAG GAA ATA GCT Lys Glu Glu Tyr Glu Ala Ala Arg Thr Val Leu Gln Glu Glu Ile Ala 245 250 255 260	884
CGT GGT GCT TCC ATA CAG GAC ATT CGA GCA AGG CTA ACA AAA ACT AAT Arg Gly Ala Ser Ile Gln Asp Ile Arg Ala Arg Leu Thr Lys Thr Asn 265 270 275	932

GAT AAA AGT CAA AGC AAA GAA GAG CCT CTT CAT GTA ACA AAG AGT GAT Asp Lys Ser Gln Ser Lys Glu Glu Pro Leu His Val Thr Lys Ser Asp 280 285 290	980
ATA CCT GAT GAC CTT GCC CAA GCA CAA GCT TAC ATT AGG TGG GAG AAA Ile Pro Asp Asp Leu Ala Gln Ala Gln Ala Tyr Ile Arg Trp Glu Lys 295 300 305	1028
GCA GGA AAG CCG AAC TAT CCT CCA GAA AAG CAA ATT GAA GAA CTC GAA Ala Gly Lys Pro Asn Tyr Pro Pro Glu Lys Gln Ile Glu Glu Leu Glu 310 315 320	1076
GAA GCA AGA AGA GAA TTG CAA CTT GAG CTT GAG AAA GGC ATT ACC CTT Glu Ala Arg Arg Glu Leu Gln Leu Glu Leu Glu Lys Gly Ile Thr Leu 325 330 335 340	1124
GAT GAG TTG CGG AAA ACG ATT ACA AAA GGG GAG ATA AAA ACT AAG GTG Asp Glu Leu Arg Lys Thr Ile Thr Lys Gly Glu Ile Lys Thr Lys Val 345 350 355	1172
GAA AAG CAC CTG AAA AGA AGT TCT TTT GCC GTT GAA AGA ATC CAA AGA Glu Lys His Leu Lys Arg Ser Ser Phe Ala Val Glu Arg Ile Gln Arg 360 365 370	1220
AAG AAG AGA GAC TTT GGG CAT CTT ATT AAT AAG TAT ACT TCC AGT CCT Lys Lys Arg Asp Phe Gly His Leu Ile Asn Lys Tyr Thr Ser Ser Pro 375 380 385	1268
GCA GTA CAA GTA CAA AAG GTC TTG GAA GAA CCA CCA GCC TTA TCT AAA Ala Val Gln Val Gln Lys Val Leu Glu Glu Pro Pro Ala Leu Ser Lys 390 395 400	1316
ATT AAG CTG TAT GCC AAG GAG AAG GAG GAG CAG ATT GAT GAT CCG ATC Ile Lys Leu Tyr Ala Lys Glu Lys Glu Glu Gln Ile Asp Asp Pro Ile 405 410 415 420	1364
CTA AAT AAA AAG ATC TTT AAG GTC GAT GAT GGG GAG CTA CTG GTA CTG Leu Asn Lys Lys Ile Phe Lys Val Asp Asp Gly Glu Leu Leu Val Leu 425 430 435	1412
GTA GCA AAG TCC TCT GGG AAG ACA AAA GTA CAT CTA GCT ACA GAT CTG Val Ala Lys Ser Ser Gly Lys Thr Lys Val His Leu Ala Thr Asp Leu 440 445 450	1460
AAT CAG CCA ATT ACT CTT CAC TGG GCA TTA TCC AAA AGT CCT GGA GAG Asn Gln Pro Ile Thr Leu His Trp Ala Leu Ser Lys Ser Pro Gly Glu 455 460 465	1508
TGG ATG GTA CCA CCT TCA AGC ATA TTG CCT CCT GGG TCA ATT ATT TTA Trp Met Val Pro Pro Ser Ser Ile Leu Pro Pro Gly Ser Ile Ile Leu 470 475 480	1556
GAC AAG GCT GCC GAA ACA CCT TTT TCA GCC AGT TCT TCT GAT GGT CTA Asp Lys Ala Ala Glu Thr Pro Phe Ser Ala Ser Ser Ser Asp Gly Leu 485 490 495 500	1604
ACT TCT AAG GTA CAA TCT TTG GAT ATA GTA ATT GAA GAT GGC AAT TTT Thr Ser Lys Val Gln Ser Leu Asp Ile Val Ile Glu Asp Gly Asn Phe 505 510 515	1652

GTG GGG ATG CCA TTT GTT CTT TTG TCT GGT GAA AAA TGG ATT AAG AAC Val Gly Met Pro Phe Val Leu Leu Ser Gly Glu Lys Trp Ile Lys Asn 520 525 530	1700
CAA GGG TCG GAT TTC TAT GTT GGC TTC AGT GCT GCA TCC AAA TTA GCA Gln Gly Ser Asp Phe Tyr Val Gly Phe Ser Ala Ala Ser Lys Leu Ala 535 540 545	1748
CTC AAG GCT GCT GGG GAT GGC AGT GGA ACT GCA AAG TCT TTA CTG GAT Leu Lys Ala Ala Gly Asp Gly Ser Gly Thr Ala Lys Ser Leu Leu Asp 550 555 560	1796
AAA ATA GCA GAT ATG GAA AGT GAG GCT CAG AAG TCA TTT ATG CAC CGG Lys Ile Ala Asp Met Glu Ser Glu Ala Gln Lys Ser Phe Met His Arg 565 570 575 580	1844
TTT AAT ATT GCA GCT GAC TTG ATA GAA GAT GCC ACT AGT GCT GGT GAA Phe Asn Ile Ala Ala Asp Leu Ile Glu Asp Ala Thr Ser Ala Gly Glu 585 590 595	1892
CTT GGT TTT GCT GGA ATT CTT GTA TGG ATG AGG TTC ATG GCT ACA AGG Leu Gly Phe Ala Gly Ile Leu Val Trp Met Arg Phe Met Ala Thr Arg 600 605 610	1940
CAA CTG ATA TGG AAC AAA AAC TAT AAC GTA AAA CCA CGT GAA ATA AGC Gln Leu Ile Trp Asn Lys Asn Tyr Asn Val Lys Pro Arg Glu Ile Ser 615 620 625	1988
AAG GCT CAG GAC AGA CTT ACA GAC TTG TTG CAG AAT GCT TTC ACC AGT Lys Ala Gln Asp Arg Leu Thr Asp Leu Leu Gln Asn Ala Phe Thr Ser 630 635 640	2036
CAC CCT CAG TAC CGT GAA ATT TTG CGG ATG ATT ATG TCA ACT GTT GGA His Pro Gln Tyr Arg Glu Ile Leu Arg Met Ile Met Ser Thr Val Glu 645 650 655 660	2084
CGT GGA GGT GAA GGG GAT GTA GGA CAG CGA ATT AGG GAT GAA ATT TTG Arg Gly Gly Glu Gly Asp Val Gly Gln Arg Ile Arg Asp Glu Ile Leu 665 670 675	2132
GTC ATC CAG AGG AAC AAT GAC TGC AAG GGT GGT ATG ATG CAA GAA TGG Val Ile Gln Arg Asn Asn Asp Cys Lys Gly Gly Met Met Gln Glu Trp 680 685 690	2180
CAT CAG AAA TTG CAT AAT AAT ACT AGT CCT GAT GAT GTT GTG ATC TGT His Gln Lys Leu His Asn Asn Thr Ser Pro Asp Asp Val Val Ile Cys 695 700 705	2228
CAG GCA TTA ATT GAC TAC ATC AAG AGT GAT TTT GAT CTT GGT GTT TAT Gln Ala Leu Ile Asp Tyr Ile Lys Ser Asp Phe Asp Leu Gly Val Tyr 710 715 720	2276
TGG AAA ACC CTG AAT GAG AAC GGA ATA ACA AAA GAG CGT CTT TTG AGT Trp Lys Thr Leu Asn Glu Asn Gly Ile Thr Lys Glu Arg Leu Leu Ser 725 730 735 740	2324
TAT GAC CGT GCT ATC CAT TCT GAA CCA AAT TTT AGA GGA GAT CAA AAG Tyr Asp Arg Ala Ile His Ser Glu Pro Asn Phe Arg Gly Asp Gln Lys 745 750 755	2372

GGT GGT CTT TTG CGT GAT TTA GGT CAC TAT ATG AGA ACA TTG AAG GCA Gly Gly Leu Leu Arg Asp Leu Gly His Tyr Met Arg Thr Leu Lys Ala 760 765 770	2420
GTT CAT TCA GGT GCA GAT CTT GAG TCT GCT ATT GCA AAC TGC ATG GGC Val His Ser Gly Ala Asp Leu Glu Ser Ala Ile Ala Asn Cys Met Gly 775 780 785	2468
TAC AAA ACT GAG GGA GAA GGC TTT ATG GTT GGA GTC CAG ATA AAT CCT Tyr Lys Thr Glu Gly Glu Gly Phe Met Val Gly Val Gln Ile Asn Pro 790 795 800	2516
GTA TCA GGC TTG CCA TCT GGC TTT CAG GAC CTC CTC CAT TTT GTC TTA Val Ser Gly Leu Pro Ser Gly Phe Gln Asp Leu Leu His Phe Val Leu 805 810 815 820	2564
GAC CAT GTG GAA GAT AAA AAT GTG GAA ACT CTT CTT GAG AGA TTG CTA Asp His Val Glu Asp Lys Asn Val Glu Thr Leu Leu Glu Arg Leu Leu 825 830 835	2612
GAG GCT CGT GAG GAG CTT AGG CCC TTG CTT CTC AAA CCA AAC AAC CGT Glu Ala Arg Glu Glu Leu Arg Pro Leu Leu Leu Lys Pro Asn Asn Arg 840 845 850	2660
CTA AAG GAT CTG CTG TTT TTG GAC ATA GCA CTT GAT TCT ACA GTT AGA Leu Lys Asp Leu Leu Phe Leu Asp Ile Ala Leu Asp Ser Thr Val Arg 855 860 865	2708
ACA GCA GTA GAA AGG GGA TAT GAA GAA TTG AAC AAC GCT AAT CCT GAG Thr Ala Val Glu Arg Gly Tyr Glu Glu Leu Asn Asn Ala Asn Pro Glu 870 875 880	2756
AAA ATC ATG TAC TTC ATC TCC CTC GTT CTT GAA AAT CTC GCA CTC TCT Lys Ile Met Tyr Phe Ile Ser Leu Val Leu Glu Asn Leu Ala Leu Ser 885 890 895 900	2804
GTG GAC GAT AAT GAA GAT CTT GTT TAT TGC TTG AAG GGA TGG AAT CAA Val Asp Asp Asn Glu Asp Leu Val Tyr Cys Leu Lys Gly Trp Asn Gln 905 910 915	2852
GCT CTT TCA ATG TCC AAT GGT GGG GAC AAC CAT TGG GCT TTA TTT GCA Ala Leu Ser Met Ser Asn Gly Gly Asp Asn His Trp Ala Leu Phe Ala 920 925 930	2900
AAA GCT GTG CTT GAC AGA ACC CGT CTT GCA CTT GCA AGC AAG GCA GAG Lys Ala Val Leu Asp Arg Thr Arg Leu Ala Leu Ala Ser Lys Ala Glu 935 940 945	2948
TGG TAC CAT CAC TTA TTG CAG CCA TCT GCC GAA TAT CTA GGA TCA ATA Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly Ser Ile 950 955 960	2996
CTT GGG GTG GAC CAA TGG GCT TTG AAC ATA TTT ACT GAA GAA ATT ATA Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu Ile Ile 965 970 975 980	3044
CGT GCT GGA TCA GCA GCT TCA TTA TCC TCT CTT CTT AAT AGA CTC GAT Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg Leu Asp 985 990 995	3092

CCC GTG CTT CGG AAA ACT GCA AAT CTA GGA AGT TGG CAG ATT ATC AGT Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile Ile Ser 1000 1005 1010	3140
CCA GTT GAA GCC GTT GGA TAT GTT GTC GTT GTG GAT GAG TTG CTT TCA Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp Glu Leu Leu Ser 1015 1020 1025	3188
GTT CAG AAT GAA ATC TAC GAG AAG CCC ACG ATC TTA GTA GCA AAA TCT Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu Val Ala Lys Ser 1030 1035 1040	3236
GTT AAA GGA GAG GAG GAA ATT CCT GAT GGT GCT GTT GCC CTG ATA ACA Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val Ala Leu Ile Thr 1045 1050 1055 1060	3284
CCA GAC ATG CCA GAT GTT CTT TCA CAT GTT TCT GTT CGA GCT AGA AAT Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala Arg Asn 1065 1070 1075	3332
GGG AAG GTT TGC TTT GCT ACA TGC TTT GAT CCC AAT ATA TTG GCT GAC Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn Ile Leu Ala Asp 1080 1085 1090	3380
CTC CAA GCA AAG GAA GGA AGG ATT TTG CTC TTA AAG CCT ACA CCT TCA Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys Pro Thr Pro Ser 1095 1100 1105	3428
GAC ATA ATC TAT AGT GAG GTG AAT GAG ATT GAG CTC CAA AGT TCA AGT Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser Ser Ser 1110 1115 1120	3476
AAC TTG GTA GAA GCT GAA ACT TCA GCA ACA CTT AGA TTG GTG AAA AAG Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val Lys Lys 1125 1130 1135 1140	3524
CAA TTT GGT GGT TGT TAC GCA ATA TCA GCA GAT GAA TTC ACA AGT GAA Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu Phe Thr Ser Glu 1145 1150 1155	3572
ATG GTT GGA GCT AAA TCA CGT AAT ATT GCA TAT CTG AAA GGA AAA GTG Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu Lys Gly Lys Val 1160 1165 1170	3620
CCT TCC TCG GTG GGA ATT CCT ACG TCA GTA GCT CTT CCA TTT GGA GTC Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu Pro Phe Gly Val 1175 1180 1185	3668
TTT GAG AAA GTA CTT TCA GAC GAC ATA AAT CAG GGA GTG GCA AAA GAG Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly Val Ala Lys Glu 1190 1195 1200	3716
TTG CAA ATT CTG ATG AAA AAA CTA TCT GAA GGA GAC TTC AGC GCT CTT Leu Gln Ile Leu Met Lys Lys Leu Ser Glu Gly Asp Phe Ser Ala Leu 1205 1210 1215 1220	3764
GGT GAA ATT CGC ACA ACG GTT TTA GAT CTT TCA GCA CCA GCT CAA TTG Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Ala Pro Ala Gln Leu 1225 1230 1235	3812

GTC AAA GAG CTG AAG GAG AAG ATG CAG GGT TCT GGC ATG CCT TGG CCT	3860
Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly Met Pro Trp Pro	
1240 1245 1250	
GGT GAT GAA GGT CCA AAG CGG TGG GAA CAA GCA TGG ATG GCC ATA AAA	3908
Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp Met Ala Ile Lys	
1255 1260 1265	
AAG GTG TGG GCT TCA AAA TGG AAT GAG AGA GCA TAC TTC AGC ACA AGG	3956
Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr Phe Ser Thr Arg	
1270 1275 1280	
AAG GTG AAA CTG GAT CAT GAC TAT CTG TGC ATG GCT GTC CTT GTT CAA	4004
Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala Val Leu Val Gln	
1285 1290 1295 1300	
GAA ATA ATA AAT GCT GAT TAT GCA TTT GTC ATT CAC ACA ACC AAC CCA	4052
Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His Thr Thr Asn Pro	
1305 1310 1315	
TCT TCC GGA GAC GAC TCA GAA ATA TAT GCC GAG GTG GTC AGG GGC CTT	4100
Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val Val Arg Gly Leu	
1320 1325 1330	
GGG GAA ACA CTT GTT GGA GCT TAT CCA GGA CGT GCT TTG AGT TTT ATC	4148
Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala Leu Ser Phe Ile	
1335 1340 1345	
TGC AAG AAA AAG GAT CTC AAC TCT CCT CAA GTG TTA GGT TAC CCA AGC	4196
Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu Gly Tyr Pro Ser	
1350 1355 1360	
AAA CCG ATC GGC CTT TTC ATA AAA AGA TCT ATC ATC TTC CGA TCT GAT	4244
Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile Phe Arg Ser Asp	
1365 1370 1375 1380	
TCC AAT GGG GAA GAT TTG GAA GGT TAT GCC GGT GCT GGC CTC TAC GAC	4292
Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala Gly Leu Tyr Asp	
1385 1390 1395	
AGT GTA CCA ATG GAT GAG GAG GAA AAA GTT GTA ATT GAT TAC TCT TCC	4340
Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile Asp Tyr Ser Ser	
1400 1405 1410	
GAC CCA TTG ATA ACT GAT GGT AAC TTC CGC CAG ACA ATC CTG TCC AAC	4388
Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr Ile Leu Ser Asn	
1415 1420 1425	
ATT GCT CGT GCT GGA CAT GCT ATC GAG GAG CTA TAT GGC TCT CCT CAA	4436
Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr Gly Ser Pro Gln	
1430 1435 1440	
GAC ATT GAG GGT GTA GTG AGG GAT GGA AAG ATT TAT GTC GTT CAG ACA	4484
Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr Val Val Gln Thr	
1445 1450 1455 1460	
AGA CCA CAG ATG T GATTATATTC TCGTTGTATG TTGTTTCAGAG AAGACCACAG	4537
Arg Pro Gln Met	

ATGTGATCAT ATTCTCATTG TATCAGATCT GTGACCACTT ACCTGATACC TCCCATGAAG 4597
 TTACCTGTAT GATTATACGT GATCCAAAGC CATCACATCA TGTTACCTT CAGCTATTGG 4657
 AGGAGAAGTG AGAAGTAGGA ATTGCAATAT GAGGAATAAT AAGAAAAACT TTGTAAAAGC 4717
 TAAATTAGCT GGGTATGATA TAGGGAGAAA TGTGTAAACA TTGTACTATA TATAGTATAT 4777
 ACACACGCAT TATGTATTGC ATTATGCACT GAATAATATC GCAGCATCAA AGAAGAAATC 4837
 CTTTGGGTGG TTTCAAAA 4856

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1464 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ser Asn Ser Leu Gly Asn Asn Leu Leu Tyr Gln Gly Phe Leu Thr
 1 5 10 15
 Ser Thr Val Leu Glu His Lys Ser Arg Ile Ser Pro Pro Cys Val Gly
 20 25 30
 Gly Asn Ser Leu Phe Gln Gln Gln Val Ile Ser Lys Ser Pro Leu Ser
 35 40 45
 Thr Glu Phe Arg Gly Asn Arg Leu Lys Val Gln Lys Lys Lys Ile Pro
 50 55 60
 Met Glu Lys Lys Arg Ala Phe Ser Ser Ser Pro His Ala Val Leu Thr
 65 70 75 80
 Thr Asp Thr Ser Ser Glu Leu Ala Glu Lys Phe Ser Leu Gly Gly Asn
 85 90 95
 Ile Glu Leu Gln Val Asp Val Arg Pro Pro Thr Ser Gly Asp Val Ser
 100 105 110
 Phe Val Asp Phe Gln Val Thr Asn Gly Ser Asp Lys Leu Phe Leu His
 115 120 125
 Trp Gly Ala Val Lys Phe Gly Lys Glu Thr Trp Ser Leu Pro Asn Asp
 130 135 140
 Arg Pro Asp Gly Thr Lys Val Tyr Lys Asn Lys Ala Leu Arg Thr Pro
 145 150 155 160
 Phe Val Lys Ser Gly Ser Asn Ser Ile Leu Arg Leu Glu Ile Arg Asp
 165 170 175
 Thr Ala Ile Glu Ala Ile Glu Phe Leu Ile Tyr Asp Glu Ala His Asp
 180 185 190

Lys Trp Ile Lys Asn Asn Gly Gly Asn Phe Arg Val Lys Leu Ser Arg
 195 200 205
 Lys Glu Ile Arg Gly Pro Asp Val Ser Val Pro Glu Glu Leu Val Gln
 210 215 220
 Ile Gln Ser Tyr Leu Arg Trp Glu Arg Lys Gly Lys Gln Asn Tyr Pro
 225 230 235 240
 Pro Glu Lys Glu Lys Glu Glu Tyr Glu Ala Ala Arg Thr Val Leu Gln
 245 250 255
 Glu Glu Ile Ala Arg Gly Ala Ser Ile Gln Asp Ile Arg Ala Arg Leu
 260 265 270
 Thr Lys Thr Asn Asp Lys Ser Gln Ser Lys Glu Glu Pro Leu His Val
 275 280 285
 Thr Lys Ser Asp Ile Pro Asp Asp Leu Ala Gln Ala Gln Ala Tyr Ile
 290 295 300
 Arg Trp Glu Lys Ala Gly Lys Pro Asn Tyr Pro Pro Glu Lys Gln Ile
 305 310 315 320
 Glu Glu Leu Glu Glu Ala Arg Arg Glu Leu Gln Leu Glu Leu Glu Lys
 325 330 335
 Gly Ile Thr Leu Asp Glu Leu Arg Lys Thr Ile Thr Lys Gly Glu Ile
 340 345 350
 Lys Thr Lys Val Glu Lys His Leu Lys Arg Ser Ser Phe Ala Val Glu
 355 360 365
 Arg Ile Gln Arg Lys Lys Arg Asp Phe Gly His Leu Ile Asn Lys Tyr
 370 375 380
 Thr Ser Ser Pro Ala Val Gln Val Gln Lys Val Leu Glu Glu Pro Pro
 385 390 395 400
 Ala Leu Ser Lys Ile Lys Leu Tyr Ala Lys Glu Lys Glu Glu Gln Ile
 405 410 415
 Asp Asp Pro Ile Leu Asn Lys Lys Ile Phe Lys Val Asp Asp Gly Glu
 420 425 430
 Leu Leu Val Leu Val Ala Lys Ser Ser Gly Lys Thr Lys Val His Leu
 435 440 445
 Ala Thr Asp Leu Asn Gln Pro Ile Thr Leu His Trp Ala Leu Ser Lys
 450 455 460
 Ser Pro Gly Glu Trp Met Val Pro Pro Ser Ser Ile Leu Pro Pro Gly
 465 470 475 480
 Ser Ile Ile Leu Asp Lys Ala Ala Glu Thr Pro Phe Ser Ala Ser Ser
 485 490 495
 Ser Asp Gly Leu Thr Ser Lys Val Gln Ser Leu Asp Ile Val Ile Glu
 500 505 510

Asp	Gly	Asn	Phe	Val	Gly	Met	Pro	Phe	Val	Leu	Leu	Ser	Gly	Glu	Lys	515	520	525
Trp	Ile	Lys	Asn	Gln	Gly	Ser	Asp	Phe	Tyr	Val	Gly	Phe	Ser	Ala	Ala	530	535	540
Ser	Lys	Leu	Ala	Leu	Lys	Ala	Ala	Gly	Asp	Gly	Ser	Gly	Thr	Ala	Lys	545	550	555
Ser	Leu	Leu	Asp	Lys	Ile	Ala	Asp	Met	Glu	Ser	Glu	Ala	Gln	Lys	Ser	565	570	575
Phe	Met	His	Arg	Phe	Asn	Ile	Ala	Ala	Asp	Leu	Ile	Glu	Asp	Ala	Thr	580	585	590
Ser	Ala	Gly	Glu	Leu	Gly	Phe	Ala	Gly	Ile	Leu	Val	Trp	Met	Arg	Phe	595	600	605
Met	Ala	Thr	Arg	Gln	Leu	Ile	Trp	Asn	Lys	Asn	Tyr	Asn	Val	Lys	Pro	610	615	620
Arg	Glu	Ile	Ser	Lys	Ala	Gln	Asp	Arg	Leu	Thr	Asp	Leu	Leu	Gln	Asn	625	630	635
Ala	Phe	Thr	Ser	His	Pro	Gln	Tyr	Arg	Glu	Ile	Leu	Arg	Met	Ile	Met	645	650	655
Ser	Thr	Val	Gly	Arg	Gly	Gly	Glu	Gly	Asp	Val	Gly	Gln	Arg	Ile	Arg	660	665	670
Asp	Glu	Ile	Leu	Val	Ile	Gln	Arg	Asn	Asn	Asp	Cys	Lys	Gly	Gly	Met	675	680	685
Met	Gln	Glu	Trp	His	Gln	Lys	Leu	His	Asn	Asn	Thr	Ser	Pro	Asp	Asp	690	695	700
Val	Val	Ile	Cys	Gln	Ala	Leu	Ile	Asp	Tyr	Ile	Lys	Ser	Asp	Phe	Asp	705	710	715
Leu	Gly	Val	Tyr	Trp	Lys	Thr	Leu	Asn	Glu	Asn	Gly	Ile	Thr	Lys	Glu	725	730	735
Arg	Leu	Leu	Ser	Tyr	Asp	Arg	Ala	Ile	His	Ser	Glu	Pro	Asn	Phe	Arg	740	745	750
Gly	Asp	Gln	Lys	Gly	Gly	Leu	Leu	Arg	Asp	Leu	Gly	His	Tyr	Met	Arg	755	760	765
Thr	Leu	Lys	Ala	Val	His	Ser	Gly	Ala	Asp	Leu	Glu	Ser	Ala	Ile	Ala	770	775	780
Asn	Cys	Met	Gly	Tyr	Lys	Thr	Glu	Gly	Glu	Gly	Phe	Met	Val	Gly	Val	785	790	795
Gln	Ile	Asn	Pro	Val	Ser	Gly	Leu	Pro	Ser	Gly	Phe	Gln	Asp	Leu	Leu	805	810	815
His	Phe	Val	Leu	Asp	His	Val	Glu	Asp	Lys	Asn	Val	Glu	Thr	Leu	Leu	820	825	830

Glu Arg Leu Leu Glu Ala Arg Glu Glu Leu Arg Pro Leu Leu Leu Lys
835 840 845

Pro Asn Asn Arg Leu Lys Asp Leu Leu Phe Leu Asp Ile Ala Leu Asp
850 855 860

Ser Thr Val Arg Thr Ala Val Glu Arg Gly Tyr Glu Glu Leu Asn Asn
865 870 875 880

Ala Asn Pro Glu Lys Ile Met Tyr Phe Ile Ser Leu Val Leu Glu Asn
885 890 895

Leu Ala Leu Ser Val Asp Asp Asn Glu Asp Leu Val Tyr Cys Leu Lys
900 905 910

Gly Trp Asn Gln Ala Leu Ser Met Ser Asn Gly Gly Asp Asn His Trp
915 920 925

Ala Leu Phe Ala Lys Ala Val Leu Asp Arg Thr Arg Leu Ala Leu Ala
930 935 940

Ser Lys Ala Glu Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr
945 950 955 960

Leu Gly Ser Ile Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr
965 970 975

Glu Glu Ile Ile Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu
980 985 990

Asn Arg Leu Asp Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp
995 1000 1005

Gln Ile Ile Ser Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp
1010 1015 1020

Glu Leu Leu Ser Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu
1025 1030 1035 1040

Val Ala Lys Ser Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val
1045 1050 1055

Ala Leu Ile Thr Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val
1060 1065 1070

Arg Ala Arg Asn Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn
1075 1080 1085

Ile Leu Ala Asp Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys
1090 1095 1100

Pro Thr Pro Ser Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu
1105 1110 1115 1120

Gln Ser Ser Ser Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg
1125 1130 1135

Leu Val Lys Lys Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu
1140 1145 1150

Phe Thr Ser Glu Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu
1155 1160 1165

Lys Gly Lys Val Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu
1170 1175 1180

Pro Phe Gly Val Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly
1185 1190 1195 1200

Val Ala Lys Glu Leu Gln Ile Leu Met Lys Lys Leu Ser Glu Gly Asp
1205 1210 1215

Phe Ser Ala Leu Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Ala
1220 1225 1230

Pro Ala Gln Leu Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly
1235 1240 1245

Met Pro Trp Pro Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp
1250 1255 1260

Met Ala Ile Lys Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr
1265 1270 1275 1280

Phe Ser Thr Arg Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala
1285 1290 1295

Val Leu Val Gln Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His
1300 1305 1310

Thr Thr Asn Pro Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val
1315 1320 1325

Val Arg Gly Leu Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala
1330 1335 1340

Leu Ser Phe Ile Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu
1345 1350 1355 1360

Gly Tyr Pro Ser Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile
1365 1370 1375

Phe Arg Ser Asp Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala
1380 1385 1390

Gly Leu Tyr Asp Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile
1395 1400 1405

Asp Tyr Ser Ser Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr
1410 1415 1420

Ile Leu Ser Asn Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr
1425 1430 1435 1440

Gly Ser Pro Gln Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr
1445 1450 1455

Val Val Gln Thr Arg Pro Gln Met
1460

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1918 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Solanum tuberosum
- (B) STRAIN: C.V. Desiree

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:1..1555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCA GAG TGG TAC CAT CAC TTA TTG CAG CCA TCT GCC GAA TAT CTA GGA	48
Ala Glu Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly	
1 5 10 15	
TCA ATA CTT GGG GTG GAC CAA TGG GCT TTG AAC ATA TTT ACT GAA GAA	96
Ser Ile Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu	
20 25 30	
ATT ATA CGT GCT GGA TCA GCA GCT TCA TTA TCC TCT CTT CTT AAT AGA	144
Ile Ile Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg	
35 40 45	
CTC GAT CCC GTG CTT CGG AAA ACT GCA AAT CTA GGA AGT TGG CAG ATT	192
Leu Asp Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile	
50 55 60	
ATC AGT CCA GTT GAA GCC GTT GGA TAT GTT GTC GTT GTG GAT GAG TTG	240
Ile Ser Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp Glu Leu	
65 70 75 80	
CTT TCA GTT CAG AAT GAA ATC TAC GAG AAG CCC ACG ATC TTA GTA GCA	288
Leu Ser Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu Val Ala	
85 90 95	
AAA TCT GTT AAA GGA GAG GAG GAA ATT CCT GAT GGT GCT GTT GCC CTG	336
Lys Ser Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val Ala Leu	
100 105 110	
ATA ACA CCA GAC ATG CCA GAT GTT CTT TCA CAT GTT TCT GTT CGA GCT	384
Ile Thr Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala	
115 120 125	
AGA AAT GGG AAG GTT TGC TTT GCT ACA TGC TTT GAT CCC AAT ATA TTG	432
Arg Asn Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn Ile Leu	
130 135 140	
GCT GAC CTC CAA GCA AAG GAA GGA AGG ATT TTG CTC TTA AAG CCT ACA	480
Ala Asp Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys Pro Thr	
145 150 155 160	

CCT TCA GAC ATA ATC TAT AGT GAG GTG AAT GAG ATT GAG CTC CAA AGT	528
Pro Ser Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser	
165 170 175	
TCA AGT AAC TTG GTA GAA GCT GAA ACT TCA GCA ACA CTT AGA TTG GTG	576
Ser Ser Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val	
180 185 190	
AAA AAG CAA TTT GGT GGT TGT TAC GCA ATA TCA GCA GAT GAA TTC ACA	624
Lys Lys Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu Phe Thr	
195 200 205	
AGT GAA ATG GTT GGA GCT AAA TCA CGT AAT ATT GCA TAT CTG AAA GGA	672
Ser Glu Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu Lys Gly	
210 215 220	
AAA GTG CCT TCC TCG GTG GGA ATT CCT ACG TCA GTA GCT CTT CCA TTT	720
Lys Val Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu Pro Phe	
225 230 235 240	
GGA GTC TTT GAG AAA GTA CTT TCA GAC GAC ATA AAT CAG GGA GTG GCA	768
Gly Val Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly Val Ala	
245 250 255	
AAA GAG TTG CAA ATT CTG ACA AAA AAA CTA TCT GAA GGA GAC TTT AGC	816
Lys Glu Leu Gln Ile Leu Thr Lys Lys Leu Ser Glu Gly Asp Phe Ser	
260 265 270	
GCT CTT GGT GAA ATT CGC ACA ACG GTT TTA GAT CTT TCG ACA CCA GCT	864
Ala Leu Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Thr Pro Ala	
275 280 285	
CAA TTG GTC AAA GAG CTG AAG GAG AAG ATG CAG GGT TCT GGC ATG CCT	912
Gln Leu Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly Met Pro	
290 295 300	
TGG CCT GGT GAT GAA GGT CCA AAG CGG TGG GAA CAA GCA TGG ATG GCC	960
Trp Pro Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp Met Ala	
305 310 315 320	
ATA AAA AAG GTG TGG GCT TCA AAA TGG AAT GAG AGA GCA TAC TTC AGC	1008
Ile Lys Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr Phe Ser	
325 330 335	
ACA AGG AAG GTG AAA CTG GAT CAT GAC TAT CTG TGC ATG GCT GTC CTT	1056
Thr Arg Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala Val Leu	
340 345 350	
GTT CAA GAA ATA ATA AAT GCT GAT TAT GCA TTT GTC ATT CAC ACA ACC	1104
Val Gln Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His Thr Thr	
355 360 365	
AAC CCA TCT TCC GGA GAC GAC TCA GAA ATA TAT GCC GAG GTG GTC AGG	1152
Asn Pro Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val Val Arg	
370 375 380	
GGC CTT GGG GAA ACA CTT GTT GGA GCT TAT CCA GGA CGT GCT TTG AGT	1200
Gly Leu Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala Leu Ser	
385 390 395 400	

TTT ATC TGC AAG AAA AAG GAT CTC AAC TCT CCT CAA GTG TTA GGT TAC Phe Ile Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu Gly Tyr 405 410 415	1248
CCA AGC AAA CCG ATC GGC CTT TTC ATA AAA AGA TCT ATC ATC TTC CGA Pro Ser Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile Phe Arg 420 425 430	1296
TCT GAT TCC AAT GGG GAA GAT TTG GAA GGT TAT GCC GGT GCT GGC CTC Ser Asp Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala Gly Leu 435 440 445	1344
TAC GAC AGT GTA CCA ATG GAT GAG GAG GAA AAA GTT GTA ATT GAT TAC Tyr Asp Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile Asp Tyr 450 455 460	1392
TCT TCC GAC CCA TTG ATA ACT GAT GGT AAC TTC CGC CAG ACA ATC CTG Ser Ser Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr Ile Leu 465 470 475 480	1440
TCC AAC ATT GCT CGT GCT GGA CAT GCT ATC GAG GAG CTA TAT GGC TCT Ser Asn Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr Gly Ser 485 490 495	1488
CCT CAA GAC ATT GAG GGT GTA GTG AGG GAT GGA AAG ATT TAT GTC GTT Pro Gln Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr Val Val 500 505 510	1536
CAG ACA AGA CCA CAG ATG T GATTATATTC TCGTTGTATG TTGTTTCAGAG Gln Thr Arg Pro Gln Met 515	1585
AAGACCACAG ATGTGATCAT ATTCTCATTG TATCAGATCT GTGACCACTT ACCTGATACC	1645
TCCCATGAAG TTACCTGTAT GATTATACGT GATCCAAAGC CATCACATCA TGTTACCTT	1705
CAGCTATTGG AGGAGAAGTG AGAAGTAGGA ATTGCAATAT GAGGAATAAT AAGAAAAACT	1765
TTGTAAAAGC TAAATTAGCT GGGTATGATA TAGGGAGAAA TGTGTAAACA TTGTACTATA	1825
TATAGTATAT ACACACGCAT TATGTATTGC ATTATGCACT GAATAATATC GCAGCATCAA	1885
AGAAGAAATC CTTTGGGTGG TTTCAAAAAA AAA	1918

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 518 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Ala	Glu	Trp	Tyr	His	His	Leu	Leu	Gln	Pro	Ser	Ala	Glu	Tyr	Leu	Gly
1					5				10					15	
Ser	Ile	Leu	Gly	Val	Asp	Gln	Trp	Ala	Leu	Asn	Ile	Phe	Thr	Glu	Glu
		20					25						30		

Ile Ile Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg
35 40 45

Leu Asp Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile
50 55 60

Ile Ser Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp Glu Leu
65 70 75 80

Leu Ser Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu Val Ala
85 90 95

Lys Ser Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val Ala Leu
100 105 110

Ile Thr Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala
115 120 125

Arg Asn Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn Ile Leu
130 135 140

Ala Asp Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys Pro Thr
145 150 155 160

Pro Ser Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser
165 170 175

Ser Ser Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val
180 185 190

Lys Lys Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu Phe Thr
195 200 205

Ser Glu Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu Lys Gly
210 215 220

Lys Val Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu Pro Phe
225 230 235 240

Gly Val Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly Val Ala
245 250 255

Lys Glu Leu Gln Ile Leu Thr Lys Lys Leu Ser Glu Gly Asp Phe Ser
260 265 270

Ala Leu Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Thr Pro Ala
275 280 285

Gln Leu Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly Met Pro
290 295 300

Trp Pro Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp Met Ala
305 310 315 320

Ile Lys Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr Phe Ser
325 330 335

Thr Arg Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala Val Leu
340 345 350

75

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Jens Kossmann
Ruth Lorberth
- (ii) TITLE OF INVENTION: PLANTS WHICH SYNTHESIZE A MODIFIED STARCH,
PROCESS FOR THE PRODUCTION THEREOF AND MODIFIED STARCH
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: FISH & NEAVE
(B) STREET: 1251 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10020
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) Classification:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/EP96/04109
(B) FILING DATE: 19-SEP-1996
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: DE 19547733.2
(B) FILING DATE: 20-DEC-1995
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: DE 19534759.5
(B) FILING DATE: 19-SEP-1995
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Haley Jr., James F.
(B) REGISTRATION NUMBER: 27,794
(C) REFERENCE/DOCKET NUMBER: GFB-5
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 212-596-9000
(B) TELEFAX: 212-596-9090

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4856 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Solanum tuberosum

(B) STRAIN: C.V. Berolina

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:105..4497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CATCTTCATC GAATTTCTCG AAGCTTCTTC GCTAATTTCC TGGTTTCTTC ACTCAAATC 60

GACGTTTCTA GCTGAACTTG AGTGAATTAA GCCAGTGGGA GGAT ATG AGT AAT TCC 116
Met Ser Asn Ser
1

TTA GGG AAT AAC TTG CTG TAC CAG GGA TTC CTA ACC TCA ACA GTG TTG 164
Leu Gly Asn Asn Leu Leu Tyr Gln Gly Phe Leu Thr Ser Thr Val Leu
5 10 15 20

GAA CAT AAA AGT AGA ATC AGT CCT CCT TGT GTT GGA GGC AAT TCT TTG 212
Glu His Lys Ser Arg Ile Ser Pro Pro Cys Val Gly Gly Asn Ser Leu
25 30 35

TTT CAA CAA CAA GTG ATC TCG AAA TCA CCT TTA TCA ACT GAG TTT CGA 260
Phe Gln Gln Gln Val Ile Ser Lys Ser Pro Leu Ser Thr Glu Phe Arg
40 45 50

GGT AAC AGG TTA AAG GTG CAG AAA AAG AAA ATA CCT ATG GAA AAG AAG 308
Gly Asn Arg Leu Lys Val Gln Lys Lys Lys Ile Pro Met Glu Lys Lys
55 60 65

CGT GCT TTT TCT AGT TCT CCT CAT GCT GTA CTT ACC ACT GAT ACC TCT 356
Arg Ala Phe Ser Ser Ser Pro His Ala Val Leu Thr Thr Asp Thr Ser
70 75 80

TCT GAG CTA GCA GAA AAG TTC AGT CTA GGG GGG AAT ATT GAG CTA CAG 404
Ser Glu Leu Ala Glu Lys Phe Ser Leu Gly Gly Asn Ile Glu Leu Gln
85 90 95 100

GTT GAT GTT AGG CCT CCC ACT TCA GGT GAT GTG TCC TTT GTG GAT TTT 452
Val Asp Val Arg Pro Pro Thr Ser Gly Asp Val Ser Phe Val Asp Phe
105 110 115

CAA GTA ACA AAT GGT AGT GAT AAA CTG TTT TTG CAC TGG GGG GCA GTA 500
Gln Val Thr Asn Gly Ser Asp Lys Leu Phe Leu His Trp Gly Ala Val
120 125 130

AAA TTC GGG AAA GAA ACA TGG TCT CTT CCG AAT GAT CGT CCA GAT GGG 548
Lys Phe Gly Lys Glu Thr Trp Ser Leu Pro Asn Asp Arg Pro Asp Gly
135 140 145

ACC AAA GTG TAC AAG AAC AAA GCA CTT AGA ACT CCA TTT GTT AAA TCT 596
Thr Lys Val Tyr Lys Asn Lys Ala Leu Arg Thr Pro Phe Val Lys Ser
150 155 160

GGC TCT AAC TCC ATC CTG AGA CTG GAG ATA CGA GAC ACT GCT ATC GAA 644
Gly Ser Asn Ser Ile Leu Arg Leu Glu Ile Arg Asp Thr Ala Ile Glu
165 170 175 180

GCT ATT GAG TTT CTC ATA TAC GAT GAA GCC CAC GAT AAA TGG ATA AAG 692
Ala Ile Glu Phe Leu Ile Tyr Asp Glu Ala His Asp Lys Trp Ile Lys
185 190 195

AAT	AAT	GGT	GGT	AAT	TTT	CGT	GTC	AAA	TTG	TCA	AGA	AAA	GAG	ATA	CGA	740
Asn	Asn	Gly	Gly	Asn	Phe	Arg	Val	Lys	Leu	Ser	Arg	Lys	Glu	Ile	Arg	
		200						205					210			
GGC	CCA	GAT	GTT	TCT	GTT	CCT	GAG	GAG	CTT	GTA	CAG	ATC	CAA	TCA	TAT	788
Gly	Pro	Asp	Val	Ser	Val	Pro	Glu	Glu	Leu	Val	Gln	Ile	Gln	Ser	Tyr	
		215					220					225				
TTG	AGG	TGG	GAG	AGG	AAG	GGA	AAA	CAG	AAT	TAC	CCC	CCT	GAG	AAA	GAG	836
Leu	Arg	Trp	Glu	Arg	Lys	Gly	Lys	Gln	Asn	Tyr	Pro	Pro	Glu	Lys	Glu	
	230					235					240					
AAG	GAG	GAA	TAT	GAG	GCT	GCT	CGA	ACT	GTG	CTA	CAG	GAG	GAA	ATA	GCT	884
Lys	Glu	Glu	Tyr	Glu	Ala	Ala	Arg	Thr	Val	Leu	Gln	Glu	Glu	Ile	Ala	
	245				250					255					260	
CGT	GGT	GCT	TCC	ATA	CAG	GAC	ATT	CGA	GCA	AGG	CTA	ACA	AAA	ACT	AAT	932
Arg	Gly	Ala	Ser	Ile	Gln	Asp	Ile	Arg	Ala	Arg	Leu	Thr	Lys	Thr	Asn	
				265					270					275		
GAT	AAA	AGT	CAA	AGC	AAA	GAA	GAG	CCT	CTT	CAT	GTA	ACA	AAG	AGT	GAT	980
Asp	Lys	Ser	Gln	Ser	Lys	Glu	Glu	Pro	Leu	His	Val	Thr	Lys	Ser	Asp	
			280					285					290			
ATA	CCT	GAT	GAC	CTT	GCC	CAA	GCA	CAA	GCT	TAC	ATT	AGG	TGG	GAG	AAA	1028
Ile	Pro	Asp	Asp	Leu	Ala	Gln	Ala	Gln	Ala	Tyr	Ile	Arg	Trp	Glu	Lys	
		295					300					305				
GCA	GGA	AAG	CCG	AAC	TAT	CCT	CCA	GAA	AAG	CAA	ATT	GAA	GAA	CTC	GAA	1076
Ala	Gly	Lys	Pro	Asn	Tyr	Pro	Pro	Glu	Lys	Gln	Ile	Glu	Glu	Leu	Glu	
	310					315					320					
GAA	GCA	AGA	AGA	GAA	TTG	CAA	CTT	GAG	CTT	GAG	AAA	GGC	ATT	ACC	CTT	1124
Glu	Ala	Arg	Arg	Glu	Leu	Gln	Leu	Glu	Leu	Glu	Lys	Gly	Ile	Thr	Leu	
	325				330					335					340	
GAT	GAG	TTG	CGG	AAA	ACG	ATT	ACA	AAA	GGG	GAG	ATA	AAA	ACT	AAG	GTG	1172
Asp	Glu	Leu	Arg	Lys	Thr	Ile	Thr	Lys	Gly	Glu	Ile	Lys	Thr	Lys	Val	
				345					350					355		
GAA	AAG	CAC	CTG	AAA	AGA	AGT	TCT	TTT	GCC	GTT	GAA	AGA	ATC	CAA	AGA	1220
Glu	Lys	His	Leu	Lys	Arg	Ser	Ser	Phe	Ala	Val	Glu	Arg	Ile	Gln	Arg	
			360					365					370			
AAG	AAG	AGA	GAC	TTT	GGG	CAT	CTT	ATT	AAT	AAG	TAT	ACT	TCC	AGT	CCT	1268
Lys	Lys	Arg	Asp	Phe	Gly	His	Leu	Ile	Asn	Lys	Tyr	Thr	Ser	Ser	Pro	
		375					380					385				
GCA	GTA	CAA	GTA	CAA	AAG	GTC	TTG	GAA	GAA	CCA	CCA	GCC	TTA	TCT	AAA	1316
Ala	Val	Gln	Val	Gln	Lys	Val	Leu	Glu	Glu	Pro	Pro	Ala	Leu	Ser	Lys	
	390					395					400					
ATT	AAG	CTG	TAT	GCC	AAG	GAG	AAG	GAG	GAG	CAG	ATT	GAT	GAT	CCG	ATC	1364
Ile	Lys	Leu	Tyr	Ala	Lys	Glu	Lys	Glu	Glu	Gln	Ile	Asp	Asp	Pro	Ile	
	405				410					415					420	
CTA	AAT	AAA	AAG	ATC	TTT	AAG	GTC	GAT	GAT	GGG	GAG	CTA	CTG	GTA	CTG	1412
Leu	Asn	Lys	Lys	Ile	Phe	Lys	Val	Asp	Asp	Gly	Glu	Leu	Leu	Val	Leu	
				425				430						435		
GTA	GCA	AAG	TCC	TCT	GGG	AAG	ACA	AAA	GTA	CAT	CTA	GCT	ACA	GAT	CTG	1460
Val	Ala	Lys	Ser	Ser	Gly	Lys	Thr	Lys	Val	His	Leu	Ala	Thr	Asp	Leu	
			440					445					450			

AAT CAG CCA ATT ACT CTT CAC TGG GCA TTA TCC AAA AGT CCT GGA GAG	1508
Asn Gln Pro Ile Thr Leu His Trp Ala Leu Ser Lys Ser Pro Gly Glu	
455 460 465	
TGG ATG GTA CCA CCT TCA AGC ATA TTG CCT CCT GGG TCA ATT ATT TTA	1556
Trp Met Val Pro Pro Ser Ser Ile Leu Pro Pro Gly Ser Ile Ile Leu	
470 475 480	
GAC AAG GCT GCC GAA ACA CCT TTT TCA GCC AGT TCT TCT GAT GGT CTA	1604
Asp Lys Ala Ala Glu Thr Pro Phe Ser Ala Ser Ser Ser Asp Gly Leu	
485 490 495 500	
ACT TCT AAG GTA CAA TCT TTG GAT ATA GTA ATT GAA GAT GGC AAT TTT	1652
Thr Ser Lys Val Gln Ser Leu Asp Ile Val Ile Glu Asp Gly Asn Phe	
505 510 515	
GTG GGG ATG CCA TTT GTT CTT TTG TCT GGT GAA AAA TGG ATT AAG AAC	1700
Val Gly Met Pro Phe Val Leu Leu Ser Gly Glu Lys Trp Ile Lys Asn	
520 525 530	
CAA GGG TCG GAT TTC TAT GTT GGC TTC AGT GCT GCA TCC AAA TTA GCA	1748
Gln Gly Ser Asp Phe Tyr Val Gly Phe Ser Ala Ala Ser Lys Leu Ala	
535 540 545	
CTC AAG GCT GCT GGG GAT GGC AGT GGA ACT GCA AAG TCT TTA CTG GAT	1796
Leu Lys Ala Ala Gly Asp Gly Ser Gly Thr Ala Lys Ser Leu Leu Asp	
550 555 560	
AAA ATA GCA GAT ATG GAA AGT GAG GCT CAG AAG TCA TTT ATG CAC CGG	1844
Lys Ile Ala Asp Met Glu Ser Glu Ala Gln Lys Ser Phe Met His Arg	
565 570 575 580	
TTT AAT ATT GCA GCT GAC TTG ATA GAA GAT GCC ACT AGT GCT GGT GAA	1892
Phe Asn Ile Ala Ala Asp Leu Ile Glu Asp Ala Thr Ser Ala Gly Glu	
585 590 595	
CTT GGT TTT GCT GGA ATT CTT GTA TGG ATG AGG TTC ATG GCT ACA AGG	1940
Leu Gly Phe Ala Gly Ile Leu Val Trp Met Arg Phe Met Ala Thr Arg	
600 605 610	
CAA CTG ATA TGG AAC AAA AAC TAT AAC GTA AAA CCA CGT GAA ATA AGC	1988
Gln Leu Ile Trp Asn Lys Asn Tyr Asn Val Lys Pro Arg Glu Ile Ser	
615 620 625	
AAG GCT CAG GAC AGA CTT ACA GAC TTG TTG CAG AAT GCT TTC ACC AGT	2036
Lys Ala Gln Asp Arg Leu Thr Asp Leu Leu Gln Asn Ala Phe Thr Ser	
630 635 640	
CAC CCT CAG TAC CGT GAA ATT TTG CGG ATG ATT ATG TCA ACT GTT GGA	2084
His Pro Gln Tyr Arg Glu Ile Leu Arg Met Ile Met Ser Thr Val Gly	
645 650 655 660	
CGT GGA GGT GAA GGG GAT GTA GGA CAG CGA ATT AGG GAT GAA ATT TTG	2132
Arg Gly Gly Glu Gly Asp Val Gly Gln Arg Ile Arg Asp Glu Ile Leu	
665 670 675	
GTC ATC CAG AGG AAC AAT GAC TGC AAG GGT GGT ATG ATG CAA GAA TGG	2180
Val Ile Gln Arg Asn Asn Asp Cys Lys Gly Gly Met Met Gln Glu Trp	
680 685 690	
CAT CAG AAA TTG CAT AAT AAT ACT AGT CCT GAT GAT GTT GTG ATC TGT	2228
His Gln Lys Leu His Asn Asn Thr Ser Pro Asp Asp Val Val Ile Cys	

695

700

705

CAG GCA TTA ATT GAC TAC ATC AAG AGT GAT TTT GAT CTT GGT GTT TAT Gln Ala Leu Ile Asp Tyr Ile Lys Ser Asp Phe Asp Leu Gly Val Tyr 710 715 720	2276
TGG AAA ACC CTG AAT GAG AAC GGA ATA ACA AAA GAG CGT CTT TTG AGT Trp Lys Thr Leu Asn Glu Asn Gly Ile Thr Lys Glu Arg Leu Leu Ser 725 730 735 740	2324
TAT GAC CGT GCT ATC CAT TCT GAA CCA AAT TTT AGA GGA GAT CAA AAG Tyr Asp Arg Ala Ile His Ser Glu Pro Asn Phe Arg Gly Asp Gln Lys 745 750 755	2372
GGT GGT CTT TTG CGT GAT TTA GGT CAC TAT ATG AGA ACA TTG AAG GCA Gly Gly Leu Leu Arg Asp Leu Gly His Tyr Met Arg Thr Leu Lys Ala 760 765 770	2420
GTT CAT TCA GGT GCA GAT CTT GAG TCT GCT ATT GCA AAC TGC ATG GGC Val His Ser Gly Ala Asp Leu Glu Ser Ala Ile Ala Asn Cys Met Gly 775 780 785	2468
TAC AAA ACT GAG GGA GAA GGC TTT ATG GTT GGA GTC CAG ATA AAT CCT Tyr Lys Thr Glu Gly Glu Gly Phe Met Val Gly Val Gln Ile Asn Pro 790 795 800	2516
GTA TCA GGC TTG CCA TCT GGC TTT CAG GAC CTC CTC CAT TTT GTC TTA Val Ser Gly Leu Pro Ser Gly Phe Gln Asp Leu Leu His Phe Val Leu 805 810 815 820	2564
GAC CAT GTG GAA GAT AAA AAT GTG GAA ACT CTT CTT GAG AGA TTG CTA Asp His Val Glu Asp Lys Asn Val Glu Thr Leu Leu Glu Arg Leu Leu 825 830 835	2612
GAG GCT CGT GAG GAG CTT AGG CCC TTG CTT CTC AAA CCA AAC AAC CGT Glu Ala Arg Glu Glu Leu Arg Pro Leu Leu Leu Lys Pro Asn Asn Arg 840 845 850	2660
CTA AAG GAT CTG CTG TTT TTG GAC ATA GCA CTT GAT TCT ACA GTT AGA Leu Lys Asp Leu Leu Phe Leu Asp Ile Ala Leu Asp Ser Thr Val Arg 855 860 865	2708
ACA GCA GTA GAA AGG GGA TAT GAA GAA TTG AAC AAC GCT AAT CCT GAG Thr Ala Val Glu Arg Gly Tyr Glu Glu Leu Asn Asn Ala Asn Pro Glu 870 875 880	2756
AAA ATC ATG TAC TTC ATC TCC CTC GTT CTT GAA AAT CTC GCA CTC TCT Lys Ile Met Tyr Phe Ile Ser Leu Val Leu Glu Asn Leu Ala Leu Ser 885 890 895 900	2804
GTG GAC GAT AAT GAA GAT CTT GTT TAT TGC TTG AAG GGA TGG AAT CAA Val Asp Asp Asn Glu Asp Leu Val Tyr Cys Leu Lys Gly Trp Asn Gln 905 910 915	2852
GCT CTT TCA ATG TCC AAT GGT GGG GAC AAC CAT TGG GCT TTA TTT GCA Ala Leu Ser Met Ser Asn Gly Gly Asp Asn His Trp Ala Leu Phe Ala 920 925 930	2900
AAA GCT GTG CTT GAC AGA ACC CGT CTT GCA CTT GCA AGC AAG GCA GAG Lys Ala Val Leu Asp Arg Thr Arg Leu Ala Leu Ala Ser Lys Ala Glu 935 940 945	2948
TGG TAC CAT CAC TTA TTG CAG CCA TCT GCC GAA TAT CTA GGA TCA ATA Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly Ser Ile	2996

950	CTT GGG GTG GAC CAA TGG GCT TTG AAC ATA TTT ACT GAA GAA ATT ATA Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu Ile Ile 965 970 975 980	3044
955	CGT GCT GGA TCA GCA GCT TCA TTA TCC TCT CTT CTT AAT AGA CTC GAT Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg Leu Asp 985 990 995	3092
960	CCC GTG CTT CGG AAA ACT GCA AAT CTA GGA AGT TGG CAG ATT ATC AGT Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile Ile Ser 1000 1005 1010	3140
	CCA GTT GAA GCC GTT GGA TAT GTT GTC GTT GTG GAT GAG TTG CTT TCA Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp Glu Leu Leu Ser 1015 1020 1025	3188
	GTT CAG AAT GAA ATC TAC GAG AAG CCC ACG ATC TTA GTA GCA AAA TCT Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu Val Ala Lys Ser 1030 1035 1040	3236
	GTT AAA GGA GAG GAG GAA ATT CCT GAT GGT GCT GTT GCC CTG ATA ACA Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val Ala Leu Ile Thr 1045 1050 1055 1060	3284
	CCA GAC ATG CCA GAT GTT CTT TCA CAT GTT TCT GTT CGA GCT AGA AAT Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala Arg Asn 1065 1070 1075	3332
	GGG AAG GTT TGC TTT GCT ACA TGC TTT GAT CCC AAT ATA TTG GCT GAC Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn Ile Leu Ala Asp 1080 1085 1090	3380
	CTC CAA GCA AAG GAA GGA AGG ATT TTG CTC TTA AAG CCT ACA CCT TCA Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys Pro Thr Pro Ser 1095 1100 1105	3428
	GAC ATA ATC TAT AGT GAG GTG AAT GAG ATT GAG CTC CAA AGT TCA AGT Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser Ser Ser 1110 1115 1120	3476
	AAC TTG GTA GAA GCT GAA ACT TCA GCA ACA CTT AGA TTG GTG AAA AAG Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val Lys Lys 1125 1130 1135 1140	3524
	CAA TTT GGT GGT TGT TAC GCA ATA TCA GCA GAT GAA TTC ACA AGT GAA Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu Phe Thr Ser Glu 1145 1150 1155	3572
	ATG GTT GGA GCT AAA TCA CGT AAT ATT GCA TAT CTG AAA GGA AAA GTG Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu Lys Gly Lys Val 1160 1165 1170	3620
	CCT TCC TCG GTG GGA ATT CCT ACG TCA GTA GCT CTT CCA TTT GGA GTC Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu Pro Phe Gly Val 1175 1180 1185	3668
	TTT GAG AAA GTA CTT TCA GAC GAC ATA AAT CAG GGA GTG GCA AAA GAG Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly Val Ala Lys Glu 1190 1195 1200	3716
	TTG CAA ATT CTG ATG AAA AAA CTA TCT GAA GGA GAC TTC AGC GCT CTT	3764

Leu	Gln	Ile	Leu	Met	Lys	Lys	Leu	Ser	Glu	Gly	Asp	Phe	Ser	Ala	Leu	
1205					1210					1215					1220	
GGT	GAA	ATT	CGC	ACA	ACG	GTT	TTA	GAT	CTT	TCA	GCA	CCA	GCT	CAA	TTG	3812
Gly	Glu	Ile	Arg	Thr	Thr	Val	Leu	Asp	Leu	Ser	Ala	Pro	Ala	Gln	Leu	
				1225					1230					1235		
GTC	AAA	GAG	CTG	AAG	GAG	AAG	ATG	CAG	GGT	TCT	GGC	ATG	CCT	TGG	CCT	3860
Val	Lys	Glu	Leu	Lys	Glu	Lys	Met	Gln	Gly	Ser	Gly	Met	Pro	Trp	Pro	
			1240					1245					1250			
GGT	GAT	GAA	GGT	CCA	AAG	CGG	TGG	GAA	CAA	GCA	TGG	ATG	GCC	ATA	AAA	3908
Gly	Asp	Glu	Gly	Pro	Lys	Arg	Trp	Glu	Gln	Ala	Trp	Met	Ala	Ile	Lys	
		1255					1260					1265				
AAG	GTG	TGG	GCT	TCA	AAA	TGG	AAT	GAG	AGA	GCA	TAC	TTC	AGC	ACA	AGG	3956
Lys	Val	Trp	Ala	Ser	Lys	Trp	Asn	Glu	Arg	Ala	Tyr	Phe	Ser	Thr	Arg	
	1270					1275					1280					
AAG	GTG	AAA	CTG	GAT	CAT	GAC	TAT	CTG	TGC	ATG	GCT	GTC	CTT	GTT	CAA	4004
Lys	Val	Lys	Leu	Asp	His	Asp	Tyr	Leu	Cys	Met	Ala	Val	Leu	Val	Gln	
1285					1290					1295					1300	
GAA	ATA	ATA	AAT	GCT	GAT	TAT	GCA	TTT	GTC	ATT	CAC	ACA	ACC	AAC	CCA	4052
Glu	Ile	Ile	Asn	Ala	Asp	Tyr	Ala	Phe	Val	Ile	His	Thr	Thr	Asn	Pro	
			1305						1310					1315		
TCT	TCC	GGA	GAC	GAC	TCA	GAA	ATA	TAT	GCC	GAG	GTG	GTC	AGG	GGC	CTT	4100
Ser	Ser	Gly	Asp	Asp	Ser	Glu	Ile	Tyr	Ala	Glu	Val	Val	Arg	Gly	Leu	
			1320					1325					1330			
GGG	GAA	ACA	CTT	GTT	GGA	GCT	TAT	CCA	GGA	CGT	GCT	TTG	AGT	TTT	ATC	4148
Gly	Glu	Thr	Leu	Val	Gly	Ala	Tyr	Pro	Gly	Arg	Ala	Leu	Ser	Phe	Ile	
	1335						1340					1345				
TGC	AAG	AAA	AAG	GAT	CTC	AAC	TCT	CCT	CAA	GTG	TTA	GGT	TAC	CCA	AGC	4196
Cys	Lys	Lys	Lys	Asp	Leu	Asn	Ser	Pro	Gln	Val	Leu	Gly	Tyr	Pro	Ser	
	1350					1355					1360					
AAA	CCG	ATC	GGC	CTT	TTC	ATA	AAA	AGA	TCT	ATC	ATC	TTC	CGA	TCT	GAT	4244
Lys	Pro	Ile	Gly	Leu	Phe	Ile	Lys	Arg	Ser	Ile	Ile	Phe	Arg	Ser	Asp	
1365					1370				1375						1380	
TCC	AAT	GGG	GAA	GAT	TTG	GAA	GGT	TAT	GCC	GGT	GCT	GGC	CTC	TAC	GAC	4292
Ser	Asn	Gly	Glu	Asp	Leu	Glu	Gly	Tyr	Ala	Gly	Ala	Gly	Leu	Tyr	Asp	
			1385						1390					1395		
AGT	GTA	CCA	ATG	GAT	GAG	GAG	GAA	AAA	GTT	GTA	ATT	GAT	TAC	TCT	TCC	4340
Ser	Val	Pro	Met	Asp	Glu	Glu	Glu	Lys	Val	Val	Ile	Asp	Tyr	Ser	Ser	
			1400					1405					1410			
GAC	CCA	TTG	ATA	ACT	GAT	GGT	AAC	TTC	CGC	CAG	ACA	ATC	CTG	TCC	AAC	4388
Asp	Pro	Leu	Ile	Thr	Asp	Gly	Asn	Phe	Arg	Gln	Thr	Ile	Leu	Ser	Asn	
		1415					1420					1425				
ATT	GCT	CGT	GCT	GGA	CAT	GCT	ATC	GAG	GAG	CTA	TAT	GGC	TCT	CCT	CAA	4436
Ile	Ala	Arg	Ala	Gly	His	Ala	Ile	Glu	Glu	Leu	Tyr	Gly	Ser	Pro	Gln	
	1430					1435					1440					
GAC	ATT	GAG	GGT	GTA	GTG	AGG	GAT	GGA	AAG	ATT	TAT	GTC	GTT	CAG	ACA	4484
Asp	Ile	Glu	Gly	Val	Val	Arg	Asp	Gly	Lys	Ile	Tyr	Val	Val	Gln	Thr	
1445					1450					1455				1460		

AGA CCA CAG ATG T GATTATATTC TCGTTGTATG TTGTTTCAGAG AAGACCACAG 4537
Arg Pro Gln Met

ATGTGATCAT ATTCTCATTG TATCAGATCT GTGACCACTT ACCTGATACC TCCCATGAAG 4597
TTACCTGTAT GATTATACGT GATCCAAAGC CATCACATCA TGTTACCTT CAGCTATTGG 4657
AGGAGAAGTG AGAAGTAGGA ATTGCAATAT GAGGAATAAT AAGAAAAACT TTGTAAAAGC 4717
TAAATTAGCT GGGTATGATA TAGGGAGAAA TGTGTAAACA TTGTACTATA TATAGTATAT 4777
ACACACGCAT TATGTATTGC ATTATGCACT GAATAATATC GCAGCATCAA AGAAGAAATC 4837
CTTTGGGTGG TTTCAAAAA 4856

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1464 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Ser	Asn	Ser	Leu	Gly	Asn	Asn	Leu	Leu	Tyr	Gln	Gly	Phe	Leu	Thr	1	5	10	15
Ser	Thr	Val	Leu	Glu	His	Lys	Ser	Arg	Ile	Ser	Pro	Pro	Cys	Val	Gly	20	25	30	
Gly	Asn	Ser	Leu	Phe	Gln	Gln	Gln	Val	Ile	Ser	Lys	Ser	Pro	Leu	Ser	35	40	45	
Thr	Glu	Phe	Arg	Gly	Asn	Arg	Leu	Lys	Val	Gln	Lys	Lys	Lys	Ile	Pro	50	55	60	
Met	Glu	Lys	Lys	Arg	Ala	Phe	Ser	Ser	Ser	Pro	His	Ala	Val	Leu	Thr	65	70	75	80
Thr	Asp	Thr	Ser	Ser	Glu	Leu	Ala	Glu	Lys	Phe	Ser	Leu	Gly	Gly	Asn	85	90	95	
Ile	Glu	Leu	Gln	Val	Asp	Val	Arg	Pro	Pro	Thr	Ser	Gly	Asp	Val	Ser	100	105	110	
Phe	Val	Asp	Phe	Gln	Val	Thr	Asn	Gly	Ser	Asp	Lys	Leu	Phe	Leu	His	115	120	125	
Trp	Gly	Ala	Val	Lys	Phe	Gly	Lys	Glu	Thr	Trp	Ser	Leu	Pro	Asn	Asp	130	135	140	
Arg	Pro	Asp	Gly	Thr	Lys	Val	Tyr	Lys	Asn	Lys	Ala	Leu	Arg	Thr	Pro	145	150	155	160
Phe	Val	Lys	Ser	Gly	Ser	Asn	Ser	Ile	Leu	Arg	Leu	Glu	Ile	Arg	Asp	165	170	175	
Thr	Ala	Ile	Glu	Ala	Ile	Glu	Phe	Leu	Ile	Tyr	Asp	Glu	Ala	His	Asp	180	185	190	

Trp	Ile	Lys	Asn	Gln	Gly	Ser	Asp	Phe	Tyr	Val	Gly	Phe	Ser	Ala	Ala	
530						535					540					
Ser	Lys	Leu	Ala	Leu	Lys	Ala	Ala	Gly	Asp	Gly	Ser	Gly	Thr	Ala	Lys	
545					550					555					560	
Ser	Leu	Leu	Asp	Lys	Ile	Ala	Asp	Met	Glu	Ser	Glu	Ala	Gln	Lys	Ser	
				565					570					575		
Phe	Met	His	Arg	Phe	Asn	Ile	Ala	Ala	Asp	Leu	Ile	Glu	Asp	Ala	Thr	
			580					585					590			
Ser	Ala	Gly	Glu	Leu	Gly	Phe	Ala	Gly	Ile	Leu	Val	Trp	Met	Arg	Phe	
		595					600					605				
Met	Ala	Thr	Arg	Gln	Leu	Ile	Trp	Asn	Lys	Asn	Tyr	Asn	Val	Lys	Pro	
610						615					620					
Arg	Glu	Ile	Ser	Lys	Ala	Gln	Asp	Arg	Leu	Thr	Asp	Leu	Leu	Gln	Asn	
625					630					635					640	
Ala	Phe	Thr	Ser	His	Pro	Gln	Tyr	Arg	Glu	Ile	Leu	Arg	Met	Ile	Met	
				645					650					655		
Ser	Thr	Val	Gly	Arg	Gly	Gly	Glu	Gly	Asp	Val	Gly	Gln	Arg	Ile	Arg	
			660					665					670			
Asp	Glu	Ile	Leu	Val	Ile	Gln	Arg	Asn	Asn	Asp	Cys	Lys	Gly	Gly	Met	
		675					680					685				
Met	Gln	Glu	Trp	His	Gln	Lys	Leu	His	Asn	Asn	Thr	Ser	Pro	Asp	Asp	
	690					695					700					
Val	Val	Ile	Cys	Gln	Ala	Leu	Ile	Asp	Tyr	Ile	Lys	Ser	Asp	Phe	Asp	
705					710					715					720	
Leu	Gly	Val	Tyr	Trp	Lys	Thr	Leu	Asn	Glu	Asn	Gly	Ile	Thr	Lys	Glu	
				725					730					735		
Arg	Leu	Leu	Ser	Tyr	Asp	Arg	Ala	Ile	His	Ser	Glu	Pro	Asn	Phe	Arg	
			740					745					750			
Gly	Asp	Gln	Lys	Gly	Gly	Leu	Leu	Arg	Asp	Leu	Gly	His	Tyr	Met	Arg	
		755					760					765				
Thr	Leu	Lys	Ala	Val	His	Ser	Gly	Ala	Asp	Leu	Glu	Ser	Ala	Ile	Ala	
		770				775					780					
Asn	Cys	Met	Gly	Tyr	Lys	Thr	Glu	Gly	Glu	Gly	Phe	Met	Val	Gly	Val	
785					790					795					800	
Gln	Ile	Asn	Pro	Val	Ser	Gly	Leu	Pro	Ser	Gly	Phe	Gln	Asp	Leu	Leu	
			805						810					815		
His	Phe	Val	Leu	Asp	His	Val	Glu	Asp	Lys	Asn	Val	Glu	Thr	Leu	Leu	
			820					825					830			
Glu	Arg	Leu	Leu	Glu	Ala	Arg	Glu	Glu	Leu	Arg	Pro	Leu	Leu	Leu	Lys	
		835					840					845				
Pro	Asn	Asn	Arg	Leu	Lys	Asp	Leu	Leu	Phe	Leu	Asp	Ile	Ala	Leu	Asp	
	850					855					860					

Ser Thr Val Arg Thr Ala Val Glu Arg Gly Tyr Glu Glu Leu Asn Asn
 865 870 875 880
 Ala Asn Pro Glu Lys Ile Met Tyr Phe Ile Ser Leu Val Leu Glu Asn
 885 890 895
 Leu Ala Leu Ser Val Asp Asp Asn Glu Asp Leu Val Tyr Cys Leu Lys
 900 905 910
 Gly Trp Asn Gln Ala Leu Ser Met Ser Asn Gly Gly Asp Asn His Trp
 915 920 925
 Ala Leu Phe Ala Lys Ala Val Leu Asp Arg Thr Arg Leu Ala Leu Ala
 930 935 940
 Ser Lys Ala Glu Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr
 945 950 955 960
 Leu Gly Ser Ile Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr
 965 970 975
 Glu Glu Ile Ile Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu
 980 985 990
 Asn Arg Leu Asp Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp
 995 1000 1005
 Gln Ile Ile Ser Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp
 1010 1015 1020
 Glu Leu Leu Ser Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu
 1025 1030 1035 1040
 Val Ala Lys Ser Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val
 1045 1050 1055
 Ala Leu Ile Thr Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val
 1060 1065 1070
 Arg Ala Arg Asn Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn
 1075 1080 1085
 Ile Leu Ala Asp Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys
 1090 1095 1100
 Pro Thr Pro Ser Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu
 1105 1110 1115 1120
 Gln Ser Ser Ser Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg
 1125 1130 1135
 Leu Val Lys Lys Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu
 1140 1145 1150
 Phe Thr Ser Glu Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu
 1155 1160 1165
 Lys Gly Lys Val Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu
 1170 1175 1180
 Pro Phe Gly Val Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly
 1185 1190 1195 1200

Val Ala Lys Glu Leu Gln Ile Leu Met Lys Lys Leu Ser Glu Gly Asp
 1205 1210 1215
 Phe Ser Ala Leu Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Ala
 1220 1225 1230
 Pro Ala Gln Leu Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly
 1235 1240 1245
 Met Pro Trp Pro Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp
 1250 1255 1260
 Met Ala Ile Lys Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr
 1265 1270 1275 1280
 Phe Ser Thr Arg Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala
 1285 1290 1295
 Val Leu Val Gln Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His
 1300 1305 1310
 Thr Thr Asn Pro Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val
 1315 1320 1325
 Val Arg Gly Leu Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala
 1330 1335 1340
 Leu Ser Phe Ile Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu
 1345 1350 1355 1360
 Gly Tyr Pro Ser Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile
 1365 1370 1375
 Phe Arg Ser Asp Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala
 1380 1385 1390
 Gly Leu Tyr Asp Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile
 1395 1400 1405
 Asp Tyr Ser Ser Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr
 1410 1415 1420
 Ile Leu Ser Asn Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr
 1425 1430 1435 1440
 Gly Ser Pro Gln Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr
 1445 1450 1455
 Val Val Gln Thr Arg Pro Gln Met
 1460

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1918 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Solanum tuberosum

[illegible]

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:1..1555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCA GAG TGG TAC CAT CAC TTA TTG CAG CCA TCT GCC GAA TAT CTA GGA 48
Ala Glu Trp Tyr His His Leu Leu Gln Pro Ser Ala Glu Tyr Leu Gly
1 5 10 15

TCA ATA CTT GGG GTG GAC CAA TGG GCT TTG AAC ATA TTT ACT GAA GAA 96
Ser Ile Leu Gly Val Asp Gln Trp Ala Leu Asn Ile Phe Thr Glu Glu
20 25 30

ATT ATA CGT GCT GGA TCA GCA GCT TCA TTA TCC TCT CTT CTT AAT AGA 144
Ile Ile Arg Ala Gly Ser Ala Ala Ser Leu Ser Ser Leu Leu Asn Arg
35 40 45

CTC GAT CCC GTG CTT CGG AAA ACT GCA AAT CTA GGA AGT TGG CAG ATT 192
Leu Asp Pro Val Leu Arg Lys Thr Ala Asn Leu Gly Ser Trp Gln Ile
50 55 60

ATC AGT CCA GTT GAA GCC GTT GGA TAT GTT GTC GTT GTG GAT GAG TTG 240
Ile Ser Pro Val Glu Ala Val Gly Tyr Val Val Val Val Asp Glu Leu
65 70 75 80

CTT TCA GTT CAG AAT GAA ATC TAC GAG AAG CCC ACG ATC TTA GTA GCA 288
Leu Ser Val Gln Asn Glu Ile Tyr Glu Lys Pro Thr Ile Leu Val Ala
85 90 95

AAA TCT GTT AAA GGA GAG GAG GAA ATT CCT GAT GGT GCT GTT GCC CTG 336
Lys Ser Val Lys Gly Glu Glu Glu Ile Pro Asp Gly Ala Val Ala Leu
100 105 110

ATA ACA CCA GAC ATG CCA GAT GTT CTT TCA CAT GTT TCT GTT CGA GCT 384
Ile Thr Pro Asp Met Pro Asp Val Leu Ser His Val Ser Val Arg Ala
115 120 125

AGA AAT GGG AAG GTT TGC TTT GCT ACA TGC TTT GAT CCC AAT ATA TTG 432
Arg Asn Gly Lys Val Cys Phe Ala Thr Cys Phe Asp Pro Asn Ile Leu
130 135 140

GCT GAC CTC CAA GCA AAG GAA GGA AGG ATT TTG CTC TTA AAG CCT ACA 480
Ala Asp Leu Gln Ala Lys Glu Gly Arg Ile Leu Leu Leu Lys Pro Thr
145 150 155 160

CCT TCA GAC ATA ATC TAT AGT GAG GTG AAT GAG ATT GAG CTC CAA AGT 528
Pro Ser Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser
165 170 175

TCA AGT AAC TTG GTA GAA GCT GAA ACT TCA GCA ACA CTT AGA TTG GTG 576
Ser Ser Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val
180 185 190

AAA AAG CAA TTT GGT GGT TGT TAC GCA ATA TCA GCA GAT GAA TTC ACA 624
Lys Lys Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu Phe Thr
195 200 205

AGT GAA ATG GTT GGA GCT AAA TCA CGT AAT ATT GCA TAT CTG AAA GGA 672
Ser Glu Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu Lys Gly
210 215 220

AAA Lys 225	GTG Val	CCT Pro	TCC Ser	TCG Ser	GTG Val 230	GGA Gly	ATT Ile	CCT Pro	ACG Thr	TCA Ser 235	GTA Val	GCT Ala	CTT Leu	CCA Pro	TTT Phe 240	720
GGA Gly	GTC Val	TTT Phe	GAG Glu	AAA Lys 245	GTA Val	CTT Leu	TCA Ser	GAC Asp	GAC Asp 250	ATA Ile	AAT Asn	CAG Gln	GGA Gly	GTG Val 255	GCA Ala	768
AAA Lys	GAG Glu	TTG Leu	CAA Gln 260	ATT Ile	CTG Leu	ACA Thr	AAA Lys	AAA Lys 265	CTA Leu	TCT Ser	GAA Glu	GGA Gly	GAC Asp 270	TTT Phe	AGC Ser	816
GCT Ala	CTT Leu	GGT Gly 275	GAA Glu	ATT Ile	CGC Arg	ACA Thr	ACG Thr 280	GTT Val	TTA Leu	GAT Asp	CTT Leu	TCG Ser 285	ACA Thr	CCA Pro	GCT Ala	864
CAA Gln 290	TTG Leu	GTC Val	AAA Lys	GAG Glu	CTG Leu	AAG Lys 295	GAG Glu	AAG Lys	ATG Met	CAG Gln	GGT Gly 300	TCT Ser	GGC Gly	ATG Met	CCT Pro	912
TGG Trp 305	CCT Pro	GGT Gly	GAT Asp	GAA Glu	GGT Gly 310	CCA Pro	AAG Lys	CGG Arg	TGG Trp	GAA Glu 315	CAA Gln	GCA Ala	TGG Trp	ATG Met	GCC Ala 320	960
ATA Ile	AAA Lys	AAG Lys	GTG Val 325	TGG Trp	GCT Ala	TCA Ser	AAA Lys	TGG Trp	AAT Asn 330	GAG Glu	AGA Arg	GCA Ala	TAC Tyr	TTC Phe 335	AGC Ser	1008
ACA Thr	AGG Arg	AAG Lys	GTG Val 340	AAA Lys	CTG Leu	GAT Asp	CAT His	GAC Asp 345	TAT Tyr	CTG Leu	TGC Cys	ATG Met 350	GCT Ala	GTC Val	CTT Leu	1056
GTT Val	CAA Gln 355	GAA Glu	ATA Ile	ATA Ile	AAT Asn	GCT Ala	GAT Asp 360	TAT Tyr	GCA Ala	TTT Phe	GTC Val	ATT Ile 365	CAC His	ACA Thr	ACC Thr	1104
AAC Asn 370	CCA Pro	TCT Ser	TCC Ser	GGA Gly	GAC Asp	GAC Asp 375	TCA Ser	GAA Glu	ATA Ile	TAT Tyr 380	GCC Ala	GAG Glu	GTG Val	GTC Val	AGG Arg	1152
GGC Gly 385	CTT Leu	GGG Gly	GAA Glu	ACA Thr	CTT Leu 390	GTT Val	GGA Gly	GCT Ala	TAT Tyr	CCA Pro 395	GGA Gly	CGT Arg	GCT Ala	TTG Leu	AGT Ser 400	1200
TTT Phe	ATC Ile	TGC Cys	AAG Lys 405	AAA Lys	AAG Lys	GAT Asp	CTC Leu	AAC Asn 410	TCT Ser	CCT Pro	CAA Gln	GTG Val	TTA Leu	GGT Gly 415	TAC Tyr	1248
CCA Pro	AGC Ser	AAA Lys 420	CCG Pro	ATC Ile	GGC Gly	CTT Leu	TTC Phe	ATA Ile 425	AAA Lys	AGA Arg	TCT Ser	ATC Ile	ATC Ile 430	TTC Phe	CGA Arg	1296
TCT Ser	GAT Asp	TCC Ser 435	AAT Asn	GGG Gly	GAA Glu	GAT Asp	TTG Leu 440	GAA Glu	GGT Gly	TAT Tyr	GCC Ala	GGT Gly 445	GCT Ala	GGC Gly	CTC Leu	1344
TAC Tyr	GAC Asp 450	AGT Ser	GTA Val	CCA Pro	ATG Met	GAT Asp 455	GAG Glu	GAG Glu	GAA Glu	AAA Lys 460	GTT Val	GTA Val	ATT Ile	GAT Asp	TAC Tyr	1392
TCT Ser 465	TCC Ser	GAC Asp	CCA Pro	TTG Leu	ATA Ile 470	ACT Thr	GAT Asp	GGT Gly	AAC Asn	TTC Phe 475	CGC Arg	CAG Gln	ACA Thr	ATC Ile	CTG Leu 480	1440

Pro Ser Asp Ile Ile Tyr Ser Glu Val Asn Glu Ile Glu Leu Gln Ser
 165 170 175
 Ser Ser Asn Leu Val Glu Ala Glu Thr Ser Ala Thr Leu Arg Leu Val
 180 185 190
 Lys Lys Gln Phe Gly Gly Cys Tyr Ala Ile Ser Ala Asp Glu Phe Thr
 195 200 205
 Ser Glu Met Val Gly Ala Lys Ser Arg Asn Ile Ala Tyr Leu Lys Gly
 210 215 220
 Lys Val Pro Ser Ser Val Gly Ile Pro Thr Ser Val Ala Leu Pro Phe
 225 230 235 240
 Gly Val Phe Glu Lys Val Leu Ser Asp Asp Ile Asn Gln Gly Val Ala
 245 250 255
 Lys Glu Leu Gln Ile Leu Thr Lys Lys Leu Ser Glu Gly Asp Phe Ser
 260 265 270
 Ala Leu Gly Glu Ile Arg Thr Thr Val Leu Asp Leu Ser Thr Pro Ala
 275 280 285
 Gln Leu Val Lys Glu Leu Lys Glu Lys Met Gln Gly Ser Gly Met Pro
 290 295 300
 Trp Pro Gly Asp Glu Gly Pro Lys Arg Trp Glu Gln Ala Trp Met Ala
 305 310 315 320
 Ile Lys Lys Val Trp Ala Ser Lys Trp Asn Glu Arg Ala Tyr Phe Ser
 325 330 335
 Thr Arg Lys Val Lys Leu Asp His Asp Tyr Leu Cys Met Ala Val Leu
 340 345 350
 Val Gln Glu Ile Ile Asn Ala Asp Tyr Ala Phe Val Ile His Thr Thr
 355 360 365
 Asn Pro Ser Ser Gly Asp Asp Ser Glu Ile Tyr Ala Glu Val Val Arg
 370 375 380
 Gly Leu Gly Glu Thr Leu Val Gly Ala Tyr Pro Gly Arg Ala Leu Ser
 385 390 395 400
 Phe Ile Cys Lys Lys Lys Asp Leu Asn Ser Pro Gln Val Leu Gly Tyr
 405 410 415
 Pro Ser Lys Pro Ile Gly Leu Phe Ile Lys Arg Ser Ile Ile Phe Arg
 420 425 430
 Ser Asp Ser Asn Gly Glu Asp Leu Glu Gly Tyr Ala Gly Ala Gly Leu
 435 440 445
 Tyr Asp Ser Val Pro Met Asp Glu Glu Glu Lys Val Val Ile Asp Tyr
 450 455 460
 Ser Ser Asp Pro Leu Ile Thr Asp Gly Asn Phe Arg Gln Thr Ile Leu
 465 470 475 480
 Ser Asn Ile Ala Arg Ala Gly His Ala Ile Glu Glu Leu Tyr Gly Ser
 485 490 495

Pro Gln Asp Ile Glu Gly Val Val Arg Asp Gly Lys Ile Tyr Val Val
 500 505 510

Gln Thr Arg Pro Gln Met
 515

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